



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 09:26 AM UTC

PDB ID : 5IKZ / pdb_00005ikz
Title : Glycerol bound structure of Obc1, a bifunctional enzyme for quorum sensing-dependent oxalogenesis
Authors : Oh, J.; Rhee, S.
Deposited on : 2016-03-04
Resolution : 2.80 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

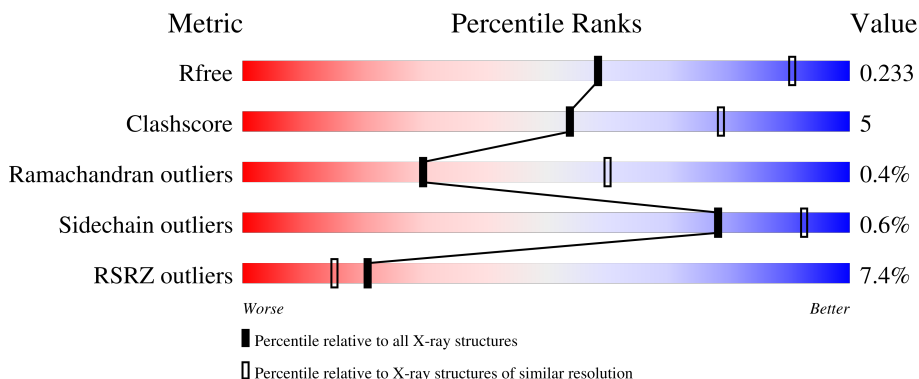
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1125	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 8062 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Oxalate biosynthetic component 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1047	Total	C	N	O	S	0	0	0
			7848	4971	1401	1459	17			

- Molecule 2 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Mg	0	0
			1	1		

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			6	3	3		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	207	Total 207	O 207	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, α , β , γ	229.97Å 229.97Å 253.76Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	46.35 – 2.80 46.35 – 2.80	Depositor EDS
% Data completeness (in resolution range)	100.0 (46.35-2.80) 100.0 (46.35-2.80)	Depositor EDS
R_{merge}	0.28	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.60 (at 2.82Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.199 , 0.227 0.205 , 0.233	Depositor DCC
R_{free} test set	3168 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	56.4	Xtriage
Anisotropy	0.138	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 69.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	8062	wwPDB-VP
Average B, all atoms (Å ²)	69.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.12% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MG, GOL

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.30	0/8025	0.73	5/10973 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	887	LYS	CA-C-N	6.04	127.38	119.84
1	A	887	LYS	C-N-CA	6.04	127.38	119.84
1	A	630	ILE	CB-CA-C	-5.17	108.87	114.35
1	A	454	GLY	CA-C-N	5.06	124.84	119.28
1	A	454	GLY	C-N-CA	5.06	124.84	119.28

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	7848	0	7541	76	0
2	A	1	0	0	0	0
3	A	6	0	8	0	0
4	A	207	0	0	5	0
All	All	8062	0	7549	76	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

All (76) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:806:HIS:HB2	1:A:832:LEU:HD12	1.56	0.85
1:A:780:TRP:HB2	1:A:832:LEU:HD21	1.68	0.76
1:A:113:PRO:HG2	1:A:151:TRP:HB3	1.71	0.71
1:A:698:ASN:HD21	1:A:702:SER:HB2	1.57	0.69
1:A:1033:ARG:HG2	1:A:1079:PRO:HA	1.74	0.69
1:A:710:ARG:NH2	1:A:1006:SER:O	2.25	0.69
1:A:315:PRO:HD2	1:A:356:ILE:HG23	1.78	0.66
1:A:35:LEU:O	1:A:40:ARG:NH2	2.28	0.66
1:A:786:THR:OG1	1:A:936:SER:OG	2.15	0.64
1:A:457:GLN:OE1	4:A:1301:HOH:O	2.15	0.64
1:A:677:ASP:O	1:A:736:ARG:NH2	2.32	0.61
1:A:573:ASP:OD1	1:A:644:ARG:NH2	2.35	0.59
1:A:613:GLU:OE2	1:A:616:ARG:NH1	2.34	0.59
1:A:780:TRP:HB2	1:A:832:LEU:CD2	2.33	0.57
1:A:610:PHE:HB2	1:A:613:GLU:HB2	1.86	0.57
1:A:587:ALA:HB3	1:A:592:LEU:HG	1.88	0.56
1:A:641:LEU:HB3	1:A:646:TYR:HB2	1.89	0.55
1:A:680:LYS:O	1:A:685:ARG:NH1	2.40	0.55
1:A:618:GLU:HG3	1:A:738:ASN:HD21	1.73	0.54
1:A:457:GLN:N	4:A:1309:HOH:O	2.39	0.53
1:A:402:ASP:OD2	1:A:431:GLN:NE2	2.41	0.53
1:A:507:GLU:OE2	1:A:510:ARG:NH1	2.42	0.52
1:A:876:TYR:HB2	1:A:944:LEU:HD22	1.92	0.52
1:A:38:ASP:OD1	1:A:39:ARG:N	2.42	0.51
1:A:28:PRO:HB2	1:A:31:LEU:HD13	1.93	0.51
1:A:518:ALA:O	1:A:522:ARG:HG3	2.10	0.51
1:A:457:GLN:NE2	4:A:1308:HOH:O	2.37	0.50
1:A:856:ARG:NH2	4:A:1312:HOH:O	2.41	0.50
1:A:856:ARG:NH1	4:A:1306:HOH:O	2.44	0.49
1:A:309:ASP:OD1	1:A:522:ARG:NH2	2.45	0.49
1:A:532:VAL:HG13	1:A:709:LEU:HD21	1.94	0.49
1:A:417:THR:HG23	1:A:420:ALA:H	1.77	0.48
1:A:857:PHE:CE1	1:A:1003:GLY:HA2	2.49	0.48
1:A:558:LEU:HD21	1:A:687:LEU:HD11	1.94	0.48
1:A:616:ARG:NH2	1:A:639:GLU:OE2	2.47	0.48
1:A:618:GLU:HG3	1:A:738:ASN:ND2	2.28	0.48
1:A:806:HIS:CB	1:A:832:LEU:HD12	2.36	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:534:LEU:HD11	1:A:564:ILE:HG23	1.96	0.47
1:A:765:ASP:N	1:A:765:ASP:OD1	2.48	0.46
1:A:12:VAL:HB	1:A:227:HIS:HB2	1.97	0.46
1:A:93:TRP:CE2	1:A:102:ARG:HG3	2.51	0.46
1:A:53:GLU:OE2	1:A:196:LYS:NZ	2.49	0.45
1:A:139:PHE:HD2	1:A:158:THR:HG23	1.80	0.45
1:A:1035:ASP:HA	1:A:1081:TRP:HE1	1.81	0.45
1:A:832:LEU:HA	1:A:832:LEU:HD23	1.71	0.44
1:A:487:VAL:HG21	1:A:492:ARG:HD3	2.00	0.44
1:A:638:ARG:NE	1:A:652:ASP:OD1	2.51	0.44
1:A:411:LYS:HE2	1:A:411:LYS:HB3	1.89	0.43
1:A:362:THR:OG1	1:A:363:LEU:N	2.51	0.43
1:A:454:GLY:HA3	1:A:455:PRO:HD3	1.78	0.43
1:A:856:ARG:HG2	1:A:978:ALA:HB2	2.00	0.43
1:A:999:ARG:HD3	1:A:1069:HIS:CD2	2.53	0.43
1:A:89:ARG:NH1	1:A:94:THR:HG22	2.34	0.43
1:A:572:GLU:OE2	1:A:644:ARG:NH1	2.52	0.43
1:A:475:GLY:HA2	1:A:497:THR:HG23	2.00	0.42
1:A:620:HIS:HA	1:A:623:LEU:HD12	2.01	0.42
1:A:151:TRP:NE1	1:A:155:ARG:O	2.42	0.42
1:A:418:ASP:O	1:A:422:GLU:HG3	2.19	0.42
1:A:996:ASN:ND2	1:A:1058:LEU:O	2.51	0.42
1:A:111:GLN:HG2	1:A:112:PRO:HD2	2.00	0.42
1:A:786:THR:HG23	1:A:852:MET:HB2	2.02	0.42
1:A:808:PHE:O	1:A:812:ILE:HG13	2.19	0.42
1:A:30:ALA:HB1	1:A:88:LEU:HD12	2.00	0.42
1:A:920:ALA:HA	1:A:923:ILE:HG13	2.01	0.42
1:A:745:GLY:HA2	1:A:874:LEU:HD13	2.00	0.42
1:A:784:PRO:HD3	1:A:835:ILE:HB	2.02	0.42
1:A:1097:GLY:O	1:A:1101:ILE:HG12	2.19	0.41
1:A:364:TYR:C	1:A:367:PRO:HD2	2.44	0.41
1:A:574:ARG:HB3	1:A:603:PHE:HE2	1.85	0.41
1:A:146:ASP:OD1	1:A:148:SER:OG	2.37	0.41
1:A:791:TYR:CE2	1:A:793:LEU:HB3	2.55	0.41
1:A:876:TYR:CD1	1:A:880:ILE:HB	2.55	0.41
1:A:849:GLU:CD	1:A:999:ARG:HH22	2.29	0.41
1:A:742:LYS:HG2	1:A:791:TYR:HB3	2.02	0.41
1:A:214:ARG:HD2	1:A:271:GLU:OE2	2.21	0.40
1:A:317:PRO:O	1:A:353:ASN:ND2	2.52	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	1033/1125 (92%)	988 (96%)	41 (4%)	4 (0%)	30	60

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	888	PRO
1	A	588	ASP
1	A	1093	PRO
1	A	918	ILE

5.3.2 Protein sidechains

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	781/922 (85%)	776 (99%)	5 (1%)	78	92

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	111	GLN
1	A	414	GLN
1	A	1033	ARG
1	A	1035	ASP
1	A	1101	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	153	HIS
1	A	481	ASN
1	A	578	HIS
1	A	724	HIS
1	A	1046	GLN
1	A	1090	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	GOL	A	1202	-	5,5,5	0.36	0	5,5,5	0.37	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GOL	A	1202	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1202	GOL	O1-C1-C2-C3
3	A	1202	GOL	O1-C1-C2-O2

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	1047/1125 (93%)	0.14	77 (7%) 20 15	32, 67, 115, 152	0

All (77) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	816	PRO	6.8
1	A	658	TYR	6.4
1	A	586	PRO	5.9
1	A	582	ALA	5.3
1	A	1106	GLN	5.2
1	A	829	PRO	4.6
1	A	2	VAL	4.6
1	A	771	LEU	4.6
1	A	1094	ALA	4.4
1	A	886	ASP	4.3
1	A	770	GLU	4.3
1	A	815	ASP	4.3
1	A	888	PRO	4.3
1	A	80	ALA	4.1
1	A	1105	LEU	4.0
1	A	654	ALA	4.0
1	A	653	ARG	4.0
1	A	657	ASP	3.9
1	A	608	ARG	3.7
1	A	1095	ASP	3.7
1	A	1096	THR	3.6
1	A	919	ASN	3.5
1	A	591	ALA	3.5
1	A	83	THR	3.5
1	A	842	ASP	3.4
1	A	898	LEU	3.4
1	A	753	THR	3.4

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Mol	Chain	Res	Type	RSRZ
1	A	610	PHE	3.3
1	A	81	SER	3.3
1	A	627	TYR	3.3
1	A	893	TYR	3.3
1	A	841	ARG	3.3
1	A	953	GLU	3.2
1	A	628	ILE	3.1
1	A	961	GLU	3.0
1	A	887	LYS	3.0
1	A	626	ARG	3.0
1	A	917	ARG	3.0
1	A	918	ILE	2.9
1	A	91	ASN	2.9
1	A	922	GLN	2.9
1	A	146	ASP	2.9
1	A	738	ASN	2.9
1	A	589	PRO	2.9
1	A	609	SER	2.9
1	A	763	ARG	2.8
1	A	895	GLU	2.7
1	A	924	GLU	2.7
1	A	75	TYR	2.7
1	A	1093	PRO	2.6
1	A	958	THR	2.6
1	A	588	ASP	2.6
1	A	581	SER	2.6
1	A	622	TYR	2.5
1	A	921	GLU	2.5
1	A	890	LYS	2.5
1	A	594	GLU	2.4
1	A	650	ALA	2.4
1	A	89	ARG	2.4
1	A	889	ALA	2.4
1	A	646	TYR	2.4
1	A	84	VAL	2.3
1	A	544	HIS	2.3
1	A	1098	ALA	2.3
1	A	655	LEU	2.3
1	A	29	HIS	2.2
1	A	587	ALA	2.2
1	A	960	ASP	2.2
1	A	590	ALA	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	624	VAL	2.2
1	A	656	GLU	2.2
1	A	629	GLN	2.2
1	A	649	GLU	2.2
1	A	831	ARG	2.1
1	A	830	LEU	2.1
1	A	1100	ALA	2.1
1	A	772	ALA	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	GOL	A	1202	6/6	0.83	0.23	70,79,86,87	0
2	MG	A	1201	1/1	0.93	0.10	77,77,77,77	0

6.5 Other polymers [i](#)

There are no such residues in this entry.